(a) transforming a *Corynebacterium* species host cell with the polynucleotide molecule of claim 2, wherein said isolated polynucleotide molecule is integrated into said host cell's chromosome, and

(b) selecting a transformed host cell.

Please substitute the following claim 7 for the pending claim 7:

7. The method of claim 6 further comprising screening for said transformed polynucleotide molecule.

Please substitute the following claim 8 for the pending claim 8:

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8. The method of claim 6 wherein said polynucleotide molecule further comprises at least one of the following:

(a) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *asd* amino acid sequence;

(b) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *dapA* amino acid sequence;

(c) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *dapB* amino acid sequence;

(d) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *ddh* amino acid sequence;

(e) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *'lysA* amino acid sequence;

(f) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *lysA* amino acid sequence; and

(g) a nucleic acid molecule encoding a *Corynebacterium* species lysine pathway *ORF2* amino acid sequence.

Please substitute the following claim 9 for the pending claim 9

9. The method of claim 8 further comprising screening for said transformed polynucleotide molecule.

Please substitute the following claim 10 for the pending claim 10.

10. The method of claim 6, wherein said isolated polynucleotide molecule further comprises at least one of the following:

(a) a nucleic acid molecule encoding the *asd* amino acid sequence of SEQ ID NO:4;

(b) a nucleic acid molecule encoding the *dapA* amino acid sequence of SEQ ID NO:6;

(c) a nucleic acid molecule encoding the *dapB* amino acid sequence of SEQ ID NO:8;

(d) a nucleic acid molecule encoding the *ddh* amino acid sequence of SEQ ID NO:10;

(e) a nucleic acid molecule encoding the *'lysA* amino acid sequence of SEQ ID NO:21;

(f) a nucleic acid molecule encoding the *lysA* amino acid sequence of SEQ ID NO:14; and

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(g) a nucleic acid molecule encoding the *ORF2* amino acid sequence of SEQ ID NO:16.

Please substitute the following claim 27 for the pending claim 27.

27. The host cell of claim 26 wherein said host cell is a *Brevibacterium* selected from the group consisting of *Brevibacterium flavum* NRRL-B30218, *Brevibacterium flavum* NRRL-B30219, *Brevibacterium lactofermentum* NRRL-B30220, *Brevibacterium lactofermentum* NRRL-B30221, *Brevibacterium lactofermentum* NRRL-B30222, *Brevibacterium flavum* NRRL-B30234 and *Brevibacterium lactofermentum* NRRL-B30235.

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Please substitute the following claim 61 for the pending claim 61.

61. The isolated polynucleotide molecule of claim 2 further comprising a promoter sequence where said promoter sequence has at least 95% sequence identity to SEQ ID NO:17, wherein said promoter sequence controls expression of said polynucleotide.

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Please substitute the following claim 63 for the pending claim 63.

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63. The isolated polynucleotide molecule of claim 61 wherein said promoter is operably directly linked to the encoded polypeptide sequence.

In the Abstract:

Please substitute the following abstract for the pending abstract.

The invention provides methods to increase the production of an amino acid from *Corynebacterium* species by way of the amplification of amino acid biosynthetic pathway genes in a host cell chromosome. In a preferred embodiment, the invention provides methods to increase the production of L-lysine in *Corynebacterium glutamicum* by way of the amplification of L-lysine biosynthetic pathway genes in a host cell chromosome. The invention also provides novel processes for the production of an amino acid by way of the amplification of amino acid biosynthetic pathway genes in a host cell chromosome and/or by increasing promoter strength. In a preferred embodiment, the invention provides processes to increase the production of L-lysine in *Corynebacterium glutamicum* by way of the amplification of L-lysine biosynthetic pathway genes in a host cell chromosome. The invention also provides novel isolated nucleic acid molecules for L-lysine biosynthetic pathway genes of *Corynebacterium glutamicum* such as a threonine-mutated, feedback-sensitive aspartokinase (*ask*), aspartate-semialdehyde dehydrogenase (*asd*), dihydrodipicolinate synthase (*dapA*), dihydrodipicolinate reductase (*dapB*), diaminopimelate dehydrogenase (*ddh*), and diaminopimelate decarboxylase (*lysA*).

In the Drawings:

Please substitute the attached Figure 13 for the pending Figure 13.